

FIG. 1

2/17

CTC TAA AGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG

100

GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA

GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC

Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser

200 CLONE 15

AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG
Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly

CLONE 8

CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu

300

TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu

CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg

400

CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly

GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly

500

AAA GAT TGG AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys

ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val

600

CGG GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr

GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val

GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg

FIG. 2A

3/17

700
AGT GGG GCC ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser

GAA GCG TCC TGA TGGGCCGCTG CTTTGCGCTG GTGGACCACA GGCATCTACA
Glu Ala Ser *

800
CAGCCTGGAC TTTGGTTCTC TCCAGGAAGG TAGCCCAGCA CTGTGAAGAC CCAGCAGGAA

GCCAGGCTGA GTGAGCCACA GACCACCTGC TTCTGAACTC AAGCTGCGTT TATTAATGCC

TCTCCCGCAC CAGGCCGGGC TTGGGCCCTG CACAGATATT TCCATTTCTT CCTCACTATG

1000
ACACTGAGCA AGATCTTGTC TCCACTAAAT GAGCTCCTGC GGGAGTAGTT GGAAAGTTGG

AACCGTGTCC AGCACAGAAG GAATCTGTGC AGATGAGCAG TCACACTGTT ACTCCACAGC

1100
GGAGGAGACC AGCTCAGAGG CCCAGGAATC GGAGCGAAGC AGAGAGGTGG AGAACTGGGA

1200
TTTGAACCCC CGCCATCCTT CACCAGAGCC CATGCTCAAC CACTGTGGCG TTCTGCTGCC

CCTGCAGTTG GCAGAAAGGA TGTTTTGTCC CATTTCTTG GAGGCCACCG GGACAGACCT

1300
GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGGTGGG

GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCTGTGT GAGTTGAGTC TCCTCTCTGA

1400
GACTGCTAAG TAGGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG

1500
CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCCTG

CAATTCTACA GTTTCTTACT GTTTTGTATC AAAATCACTA TCTTTCTGAT AACAGAATTG

1600
CCAAGGCAGC GGGATCTCGT ATCTTTAAAA AGCAGTCCTC TTATTCCTAA GGTAATCCTA

TTAAAA

FIG. 2B

hFADD	(111-145)	DWRRLARQLKVS	DTKID	SIE	DRYP	RNLT	ERV	RES	L																									
rFas	(217-251)	DAKKFARQH	KIP	ES	KIDE	EIE	HNS	PQDA	AAEQ	KIQ	LL																							
hFas	(228-262)	QVK	G	FV	R	K	N	G	V	N	E	A	K	IQ	LL																			
hTNFR-1	(341-375)	RWK	E	F	V	R	R	L	G	L	S	D	H	E	I	D	R	L	E	L	Q	N	G	R	C	L	R	E	A	Q	Y	S	M	L

hFADD	(146-180)	R	I	W	K	N	T	E	K	E	N	A	T	V	A	H	L	V	G	A	L	R	S	C	Q	M	N	L	V	A	D	L	V	Q	E	V
rFas	(252-286)	Q	C	W	Y	Q	S	H	G	K	T	G	A	C	Q	A	L	I	Q	G	L	R	K	A	N	R	C	D	I	A	E	E	I	Q	A	M
hFas	(263-297)	R	N	W	H	Q	L	H	G	K	K	E	A	Y	D	T	L	I	K	D	L	K	K	A	N	L	C	T	L	A	E	K	I	Q	T	I
hTNFR-1	(376-410)	A	T	W	R	R	R	T	P	R	R	E	A	T	L	E	L	L	G	R	V	L	R	D	M	D	L	L	G	C	L	E	D	I	E	E

FIG. 2C

5/17

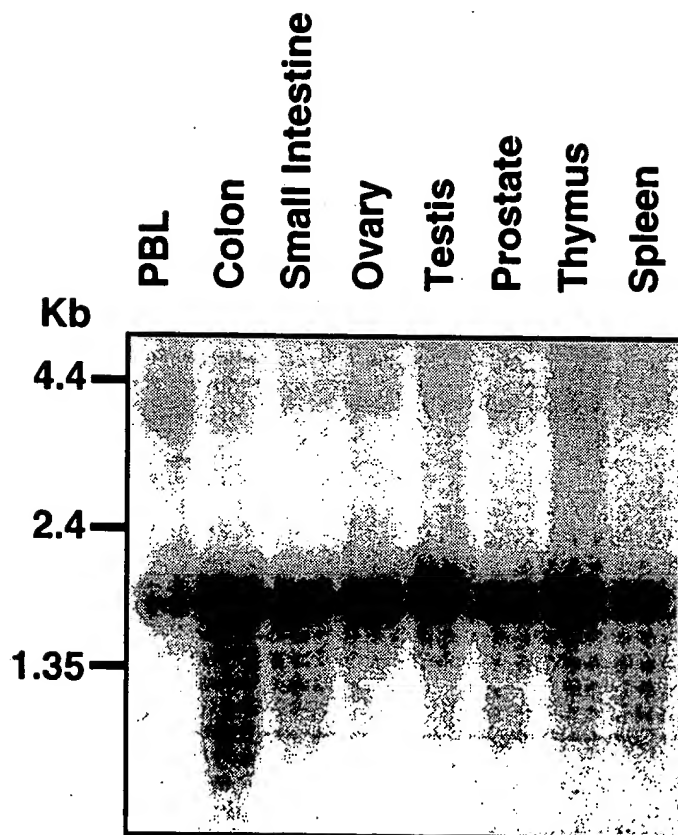


FIG. 3A

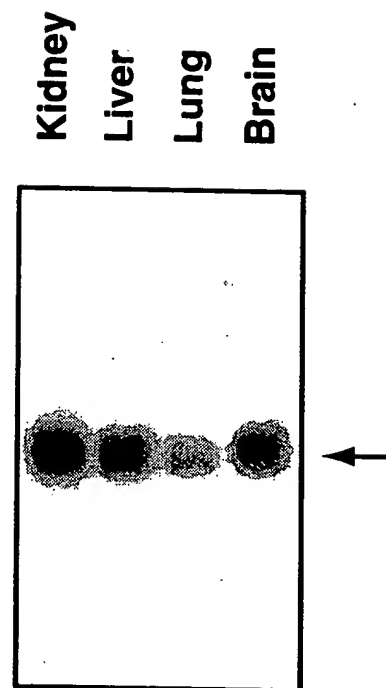


FIG. 3B

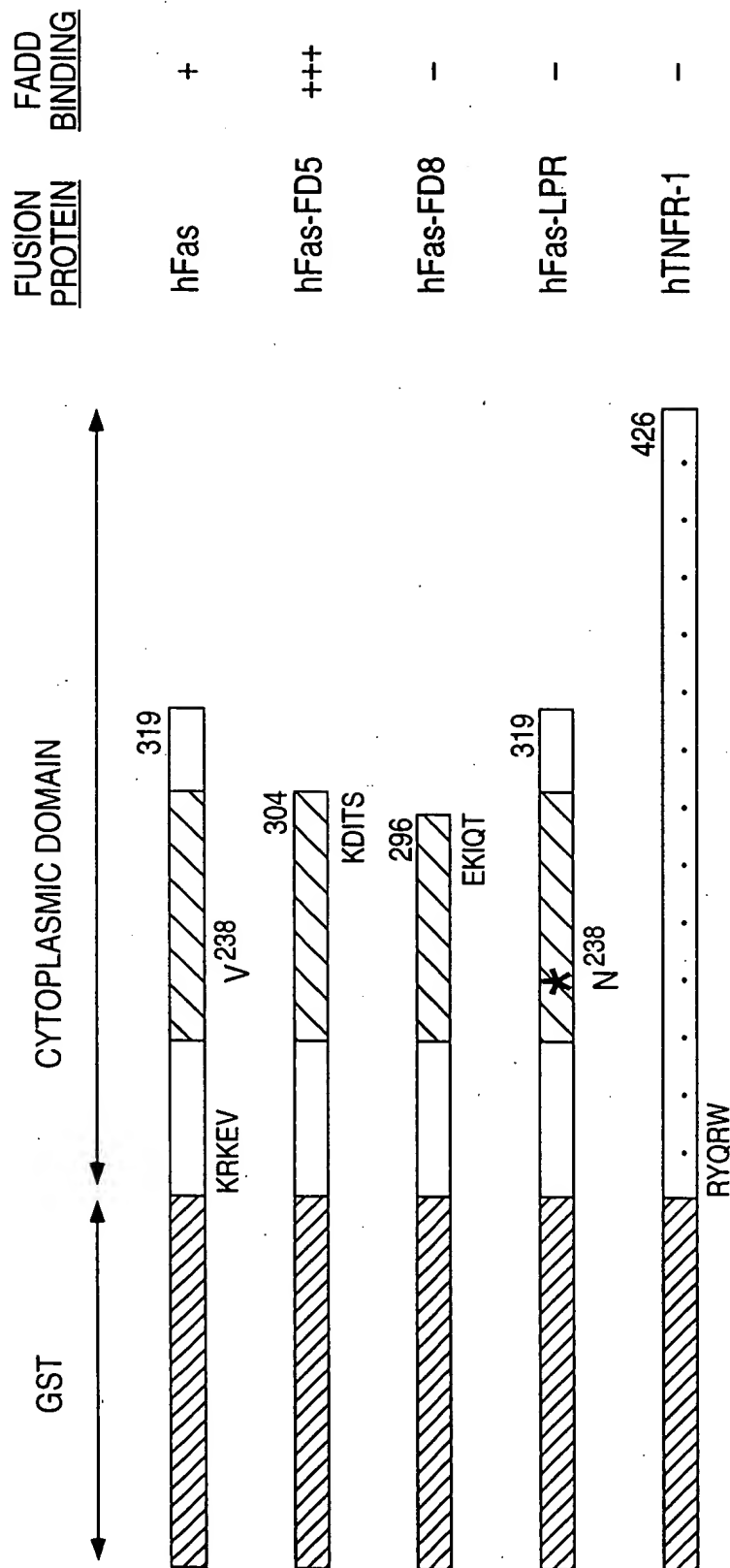


FIG. 4A

7/17

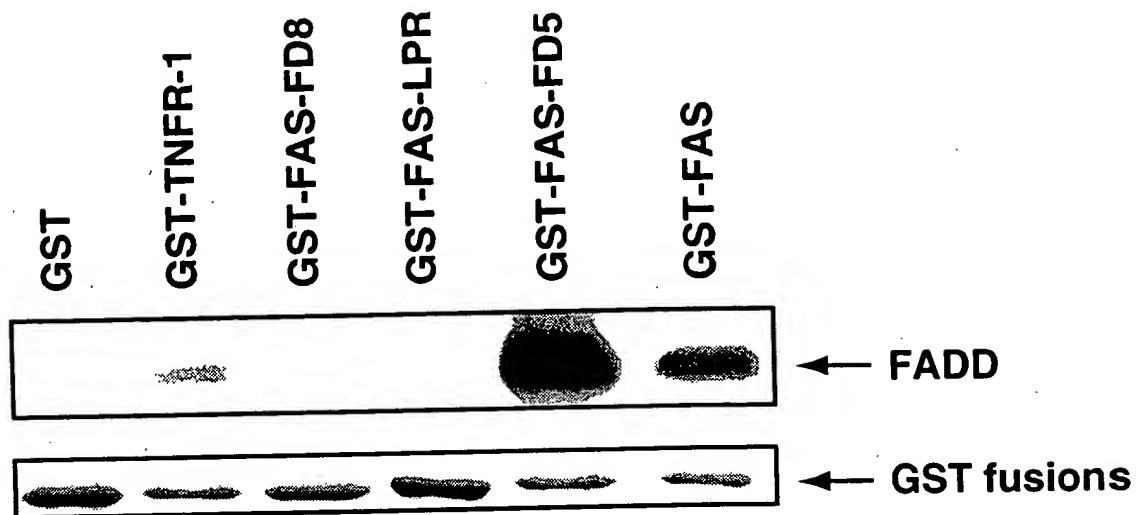


FIG. 4B

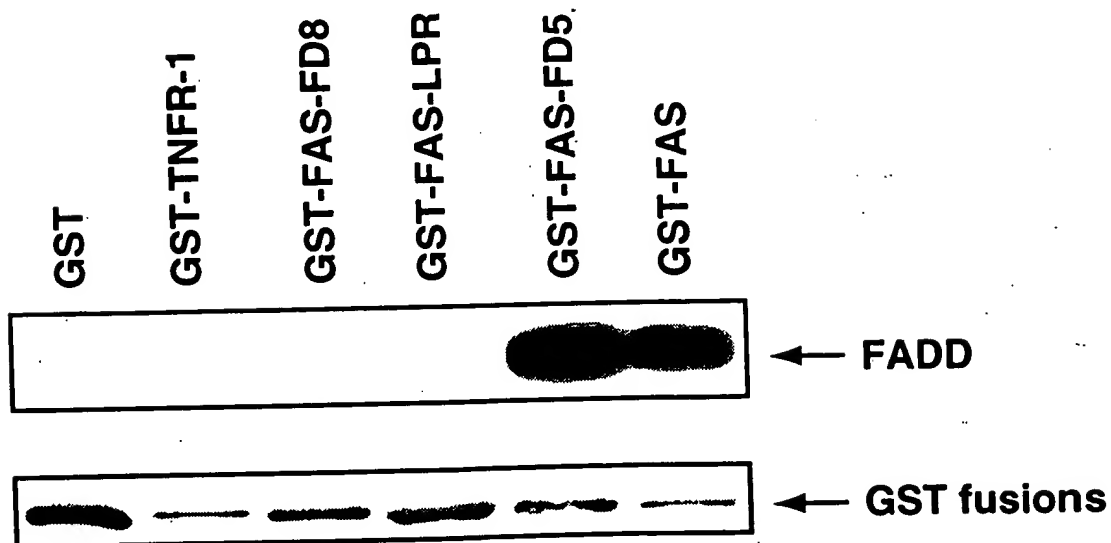


FIG. 4C

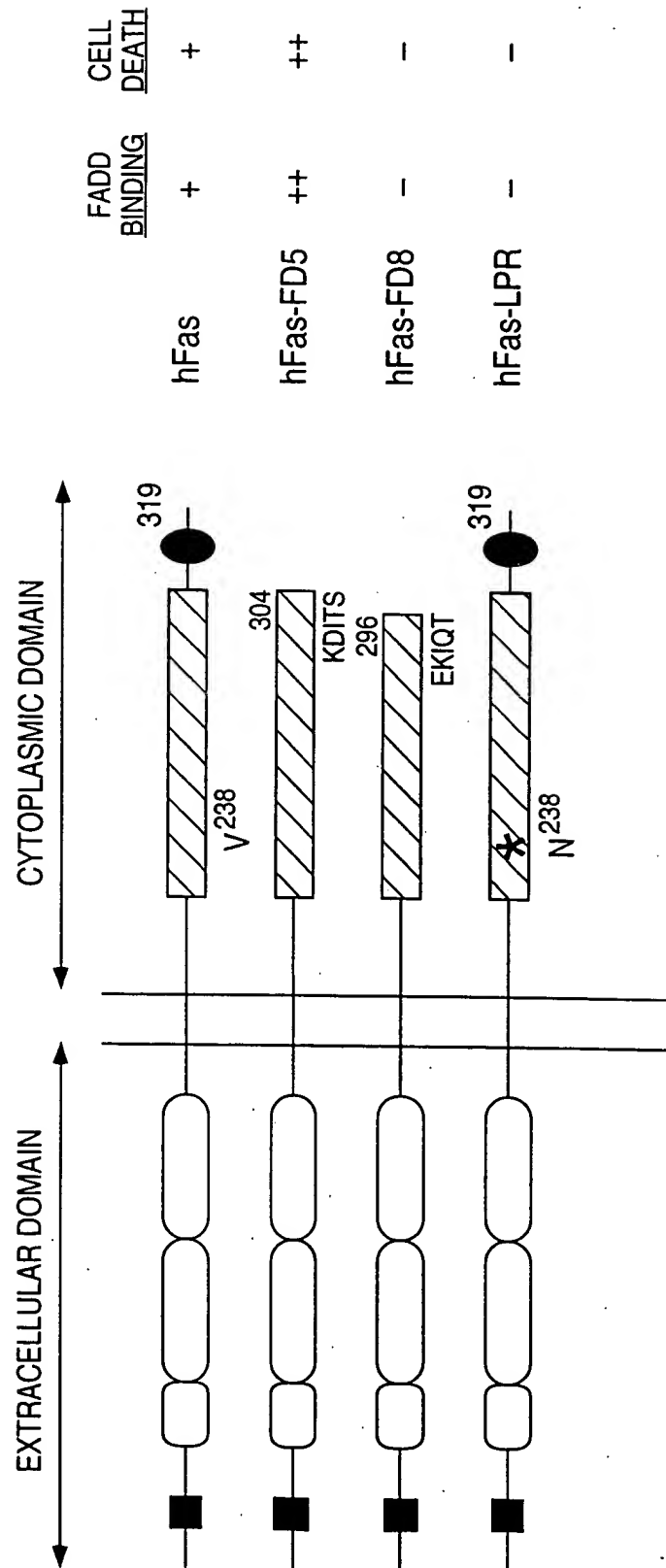


FIG. 5A

9/17

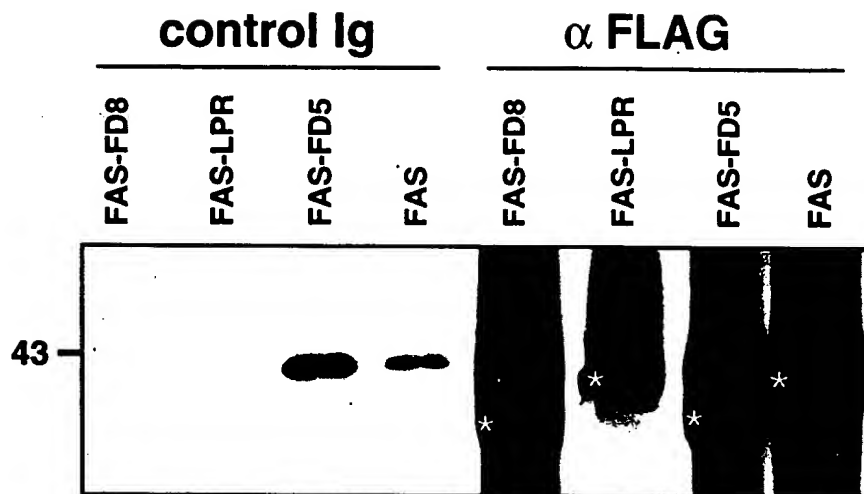
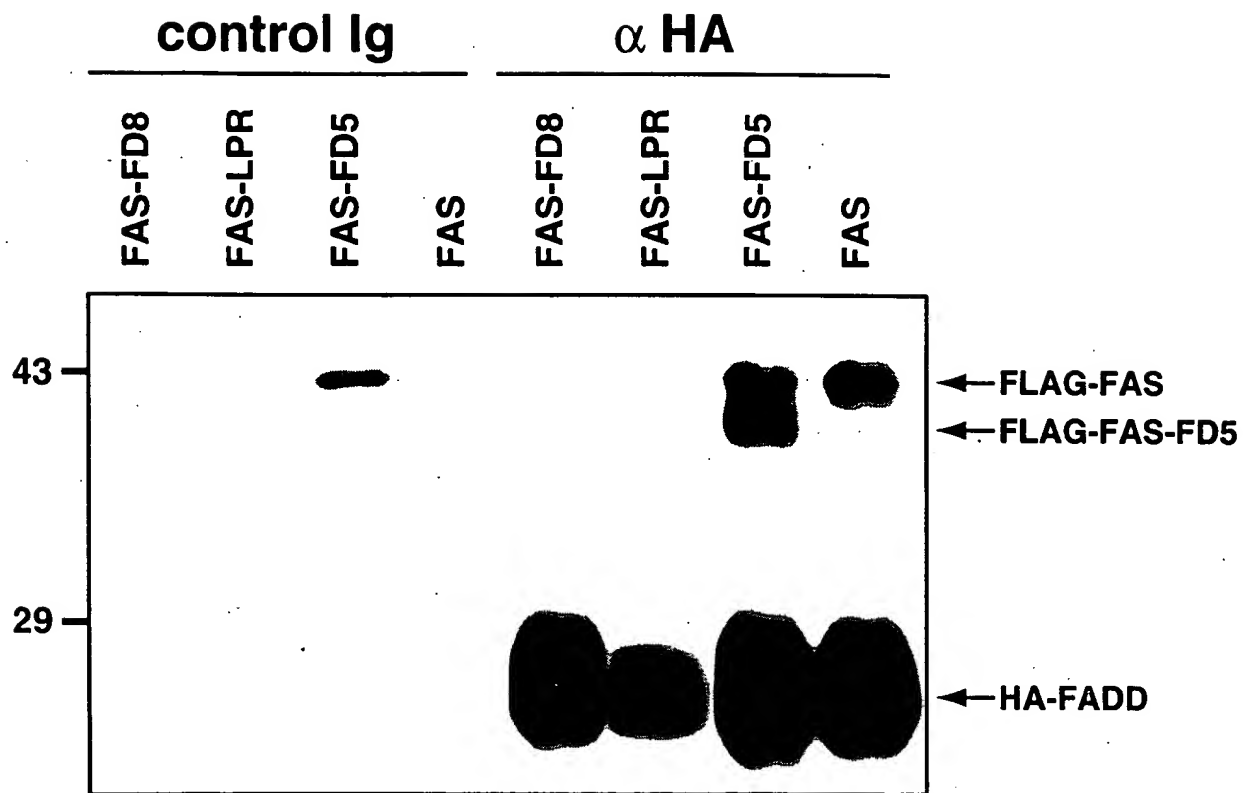


FIG. 5B

**FIG. 5C**

11/17

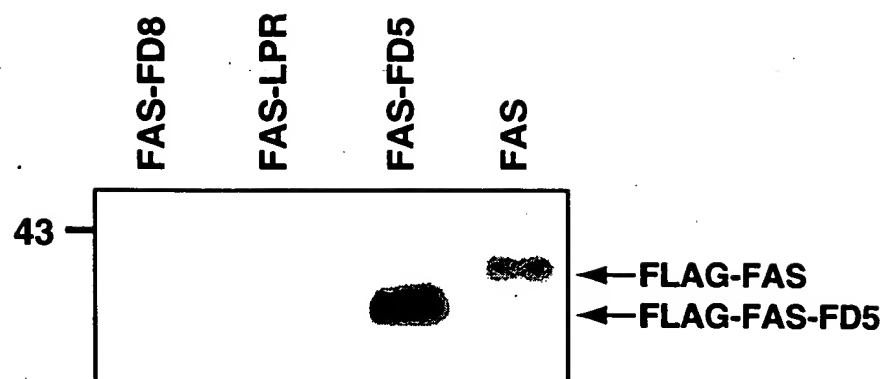


FIG. 5D

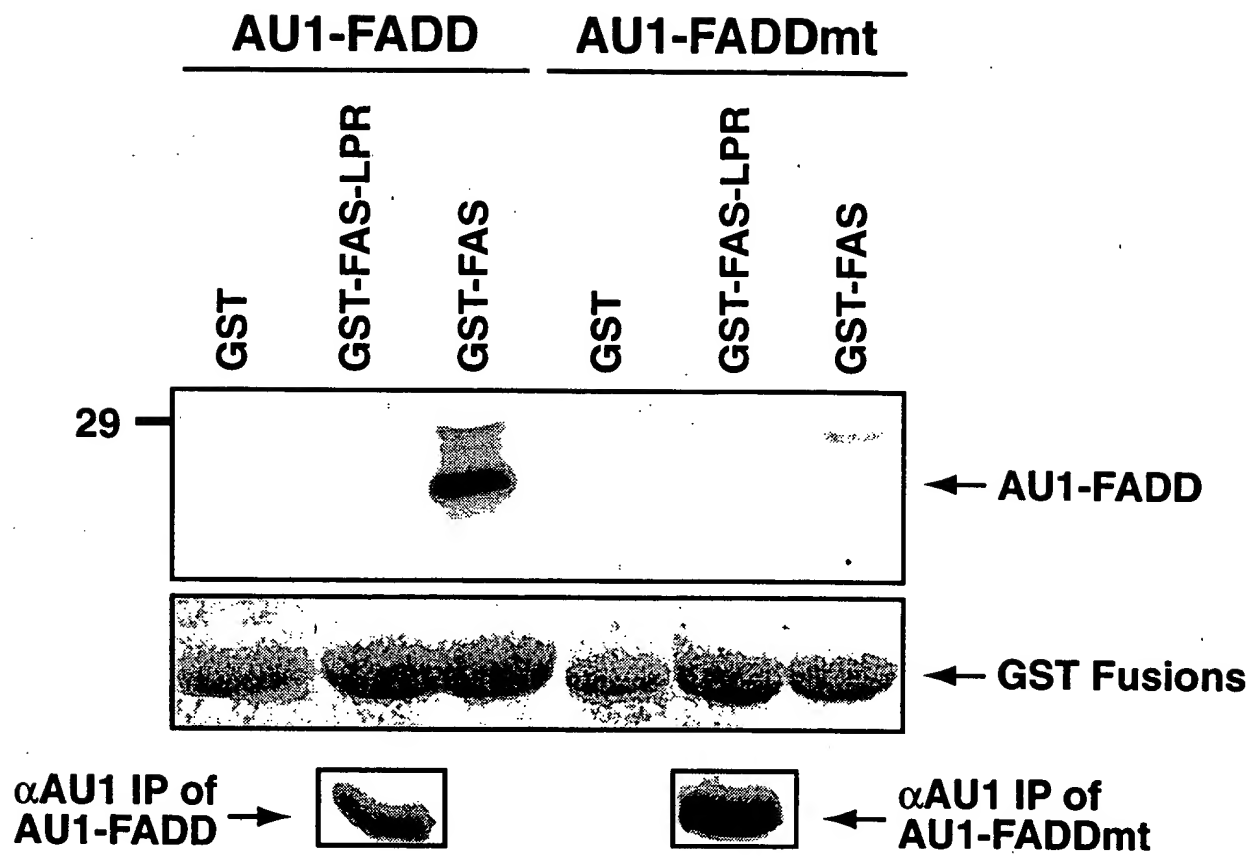


FIG. 6

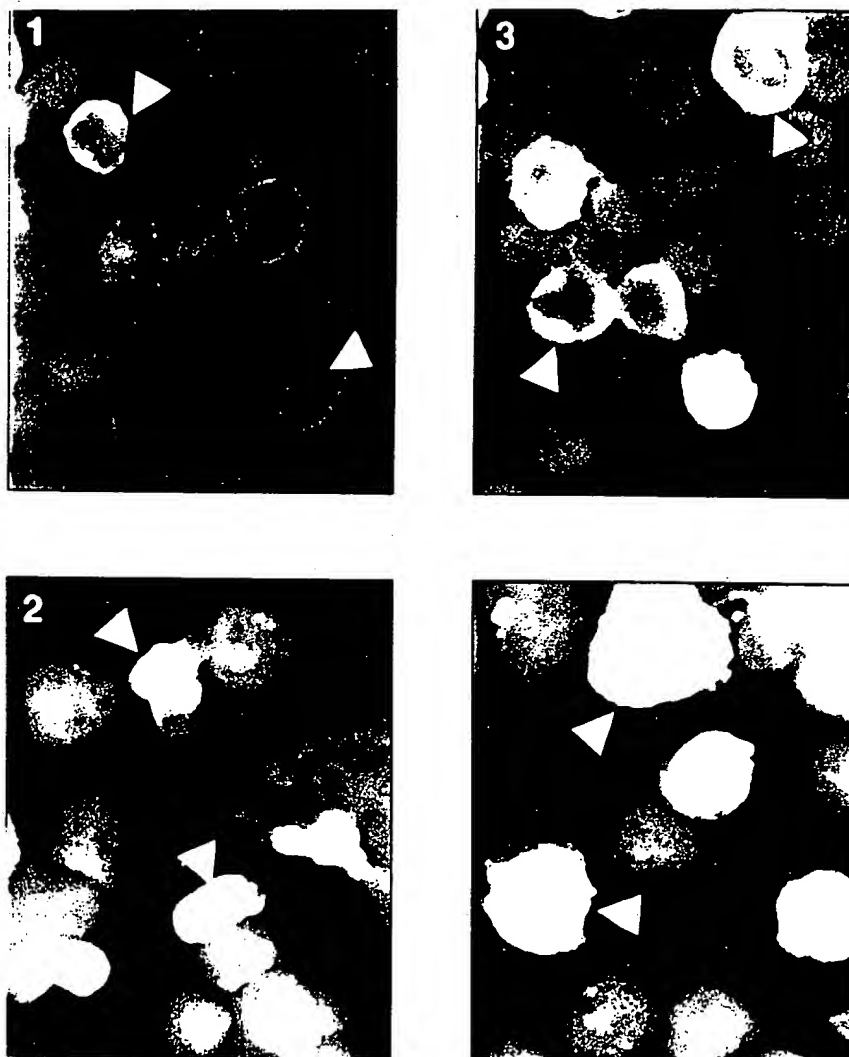


FIG. 7A

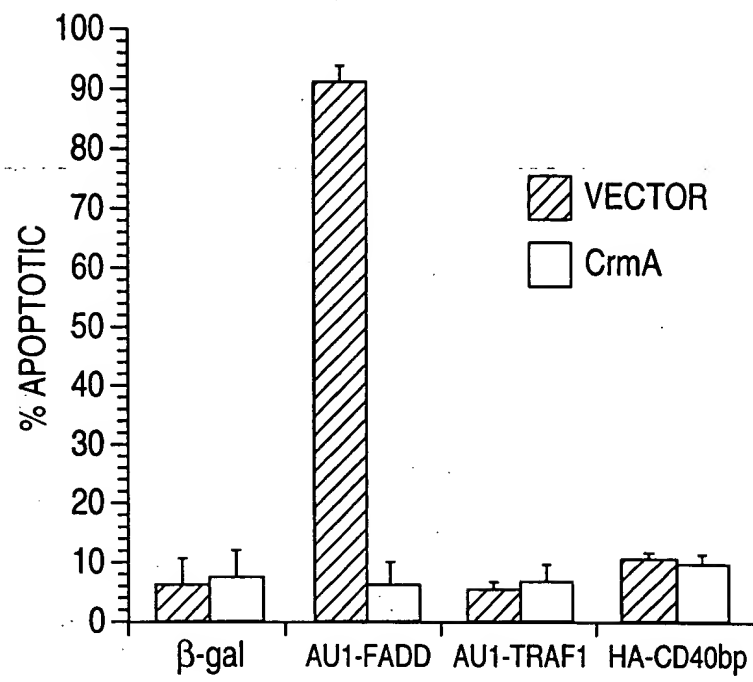
**FIG. 7B**



FIG. 7C

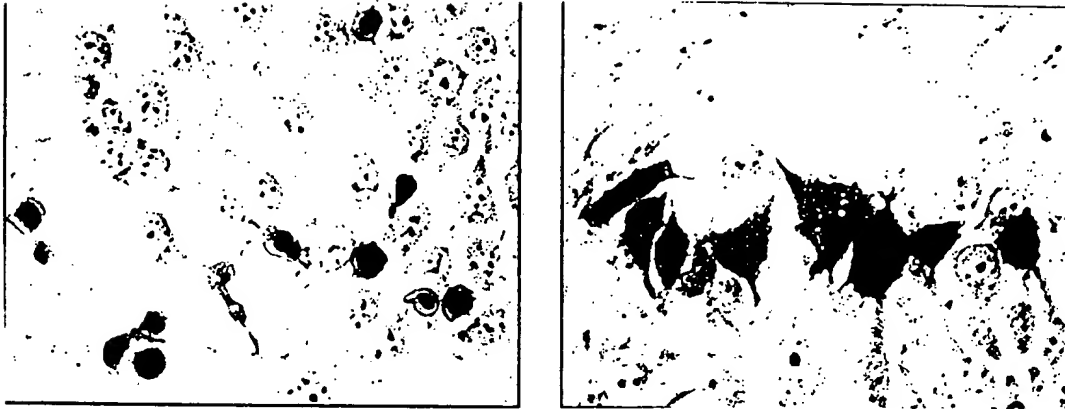


FIG. 8A

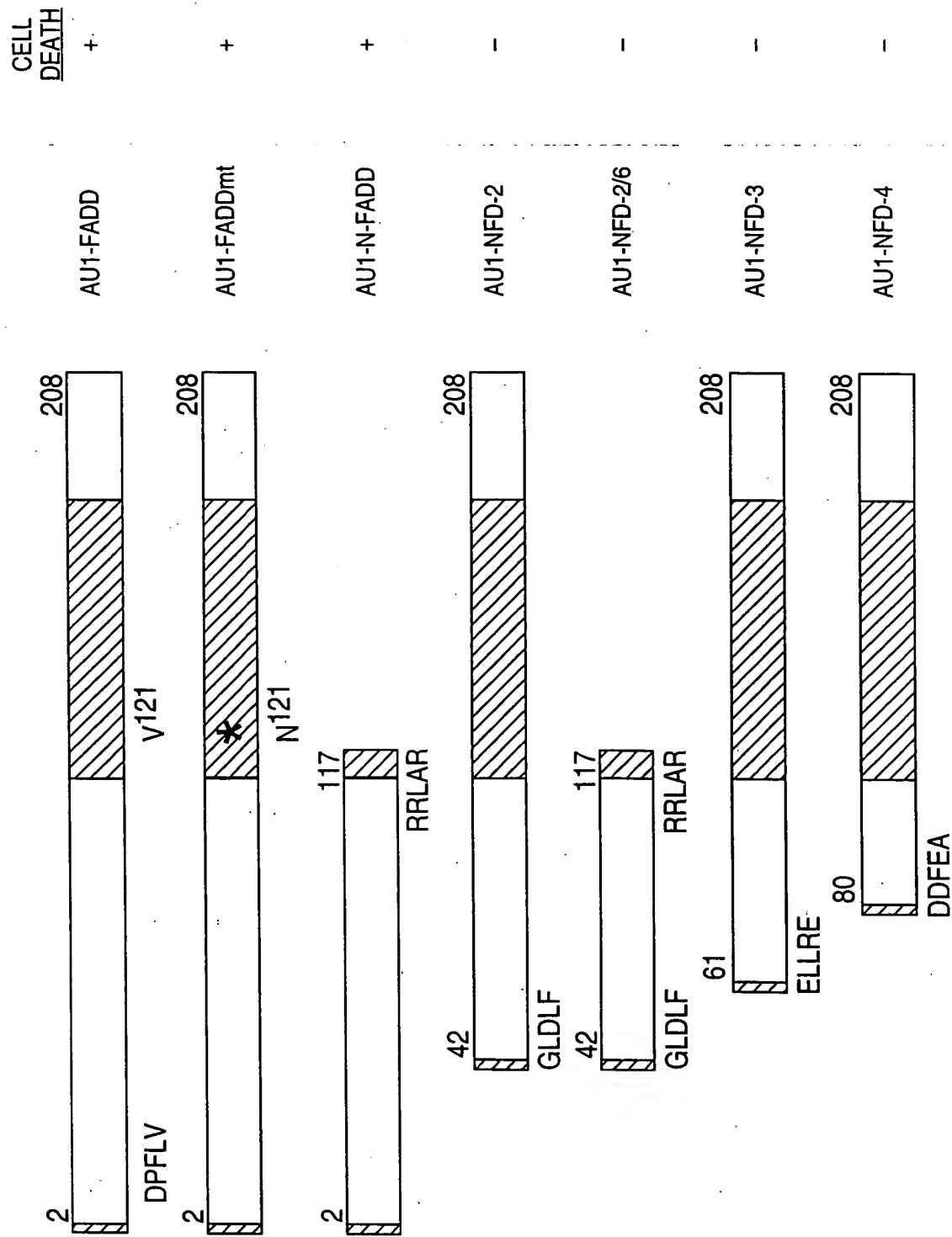


FIG. 8B